

RESULT 9

AB016068

LOCUS AB016068 2963 bp mRNA linear PRI 21-JAN-2000

DEFINITION Homo sapiens mRNA for Ste24p, complete cds.

ACCESSION AB016068

VERSION AB016068.1 GI:3721863

KEYWORDS Ste24p.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Kumagai,H., Kawamura,Y., Yanagisawa,K. and Komano,H.

TITLE Identification of a human cDNA encoding a novel protein
structurally related to the yeast membrane-associated
metalloprotease, Ste24p

JOURNAL Biochim. Biophys. Acta 1426 (3), 468-474 (1999)

PUBMED 10076063

REFERENCE 2 (bases 1 to 2963)

AUTHORS Komano,H. and Kumagai,H.

TITLE Direct Submission

JOURNAL Submitted (07-JUL-1998) Hiroto Komano, National Institute for
Longevity Sciences, Department of Dementia Research; 36-3 Gengo,
Morioka-cho, Obu, Aichi 474-8522, Japan (E-mail:hkomano@nils.go.jp,
Tel:81-562-46-2311, Fax:81-562-44-6594)

FEATURES

source

Location/Qualifiers

1..2963

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="brain"

/tissue_lib="fetal brain cDNA library"

gene

1..2963

/gene="Hs STE24"

CDS

179..1606

/gene="Hs STE24"

/codon_start=1

/product="Ste24p"

/protein_id="BAA33727.1"

/db_xref="GI:3721864"

/translation="MGMWASLDALWEMPAKKRIFGAVLLFSWTVYLWETFLAQRQRRI
YKTTTHVPPELQGIMDSETFEKSRLYQLDKSTFSFWSGLYSETGLLILFGGIPYLW
RLSGRFCGYAGFGPEYEITQSLVFLLLATLFSALTGLPWSLYNTFVIEEKHGFNQQL
GFFMKDAIKKFVVTQCILLPVSSLLLYIIKIGGDYFFIYAWLFTLVVSLVLVTIYADY
IAPLFDKFTPLPEGKLEIEVMAKSIDFPLTKVYVVEGSKRSSHSNAYFYGFFFNKR
IVLFDTLLEEYSVLNKDIQEDSGMEPRNEEENSEEIKAKVKNKKQGCKNEEVLAVLG
HELGHWKLGHTVKNIIISQMNSFLCFFLFAVLIGRKELFAAFGFYDSQPTLIGLLIIF
QFIFSPYNEVLSFCLTVLSRREFQADAFAKKL GKARDLYSALIKLNKDNLGFPVSDW
LFSMWHYSHPPLLERLQALKTMKQH"

ORIGIN

Query Match 96.9%; Score 347; DB 5; Length 2963;

Best Local Similarity 98.6%; Pred. No. 3.3e-91;

Matches 358; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

```

Qy      1 CATTATTAGCCAGATGAATTCTTTCTGTGTTTTTTTTTATTTGCTGTATTAATTGGTCG 60
          |||
Db      1225 CATTATTAGCCAGATGAATTCTTTCTGTGTTTTTTTTTATTTGCTGTATTAATTGGTCG 1284

Qy      61 AAAGGAGCTTTTGTGCAATTTGGTTTTTATGNTAGCCAACCCACTNTTATTGGACTATT 120
          |||
Db      1285 AAAGGAGCTTTTGTGCAATTTGGTTTTTATGATAGCCAACCCACTCTTATTGGACTATT 1344

Qy      121 GNTCATCTTCCAGTTTATTTTTCACCTTACAATGNGGTTCTTTCTTTTGCCTAACAGT 180
          |
Db      1345 GATCATCTTCCAGTTTATTTTTCACCTTACAATGAGGTTCTTTCTTTTGCCTAACAGT 1404

Qy      181 CCTAAGCCGCAGATTTGAGTTTCAAGCTGATGCA-TTGCCAAGAACTTGGGAAGGCTAA 239
          |||
Db      1405 CCTAAGCCGCAGATTTGAGTTTCAAGCTGATGCAATTTGCCAAGAACTTGGGAAGGCTAA 1464

```

```
Qy      240 AGACTTATATTCTGCTTTAATCAAACCTTAACAAAGATAAACTTGGGATTCCCTGTTTCTGA 299
          |||
Db      1465 AGACTTATATTCTGCTTTAATCAAACCTTAACAAAGATAAACTTGGGATTCCCTGTTTCTGA 1524

Qy      300 CTGGTTGTTCTCAATGTGGCATTATTCTCATCCTCCACTGCTAGAGAGACTTCAAGCTTT 359
          |||
Db      1525 CTGGTTGTTCTCAATGTGGCATTATTCTCATCCTCCACTGCTAGAGAGACTTCAAGCTTT 1584

Qy      360 GAA 362
          |||
Db      1585 GAA 1587
```